

1 CCAACTOCAC CTCGCTCTTA TCGATTGAAT TCCCCGGGGA TCTCTAGAG ATCCTCGAC
 61 CTGACCCAC CCCTCCGAA CCTTTCCAG CACACAACT ACGGGAGCA TTCTGATTG
 121 ATTTTGGG CTTCGATCC ACCCTCTCC CTTCCTATG GACTTGGGG ACAAGGCTC
 1 M G L W G Q S Y
 181 CCGACCGCT CCGCCCTCG AGCAGGCGC TATCCAGAG CCGAGACAG CTCGGGACC
 9 P T A E E A R A G R Y F G A R T A S Q I
 241 AGACCATGG TCTCGACCC CAAGATCCTT AAGTCTCTG TCTTCATCT CCGCTTCTG
 29 R P W L L D P K I L K F V V F I V A V L
 301 CTGCGGCTC GCGTTGACTC TCCACCCATC CCCCCAGG ACAGAGTTC CCGACAGCA
 49 L P Y R V D E A T I F R Q D E V F Q Q T
 361 GTGCCCCAC AGCAGAGAG GCGCAGCTC AAGAGAGAG AGTCTCCAG AGATCTCAT
 69 V A F Q Q Q R R S L K E E E C P A G S H
 421 AGATCAGAT ATACTGAGC CTGTACCGG TCCACAGAG GTGTGAGTA CACCATCTT
 89 R S E Y T G A C N P C T E G V D Y T I A
 481 TCCACAAAT TCGCTCTTG CCGCTATGT ACAGTTTGA AATCAGTCA AACAAATAA
 109 S M M L P S C L L C T V C K S G Q T H K
 541 AGTCTCTGA CCAGACCCAG AGACCCCTG TCTCAGTGT AAAAGAGAG CTTCAGGAT
 129 S S C T T T R D T V C Q C E K G S F Q D
 601 AAAAATCCC CTGAGATGT CCGACCTGT AGACAGGCT GTCCAGAGG GATGCTCAG
 149 K H S F E M C R T C R T G C F R G M V K
 661 GTCACTAAT GTACGCCCC GAGTGCATC AAGTCAAAA ATGAATCAG TCCAGTTC
 169 V S H C T P R S D I K C K H E S A A S S
 721 ACTGGGAAA CCGCAGCAG GAGAGAGCA GTGACCCCA TCTGGGAT CTTCTCTCT
 189 T G K T P A A E K T V T T I L G M L A S
 781 CCTATCACT ACCTTATCAT CATAGTGTG TTAGTCTAT TTTAGCTGT GGTGTGCTT
 209 P Y H Y L I I I Y V L V I I L A V V V Y
 841 GCTTTTCT GTCGGAGAA ATTCACTCT TACCTCAAAG GCATCTCTC AGTGTGGA
 229 Q F S C R K K F I S Y L K G I C S G G G
 901 GAGGCTCCG AACGTGTGA CAGATCTCT TCCGCGCGC GTTCATCTC TTCAGGTT
 249 G G F E R V E R V L F R R R S C P S R V
 961 CCGCGCGCG AGGACAATC CCGCAGCAG ACCCTGAGTA ACAGATCTT CCGCCGACC
 269 F G A E D M A R M E T L S M R Y L Q P T
 1021 CAGTCTCTG AGCAGGAAT CCAAGTCTG GAGTCCGAG AGCTAACAG TGTGCTGTA
 289 Q V S E Q K I Q G Q E L A E L T G V T V
 1081 GAGTCCGAG AGGAGCCACA GCGTCTCTG GAGAGGCGG AAGCTGAAG GTCTGAGAG
 309 X P E K F Q R L L E Q A E A E G C Q R
 1141 AGGAGGCTC TGTCTCAGT GAATGACCT GACTCCGCTG ACATCAGCAG CTCTCTGAT
 329 R R L L V F V N D A D S A D I S T L L D
 1201 GCTTCGCAA CACTGAGAG AGGACATGA AAGGAAACA TTCAGGACA ACTGCTGGC
 349 A S A T L E E G H A K E T I Q D Q L V G
 1261 TCGGAAAGC TCTTTATGA AGAAGATAG CCGGCTCTG CTACGCTCTG CTTGTGAAG
 369 S E K L F Y E E D E A G S A T S C L
 1321 AATCTCTCA GGAACCCAG CTTCCCTCA TTTACCTTT CTCTACAA GGAAGCAGC
 1381 CTGAGAGAA CAGTCCAGTA CTGACCCAT GCGCAGCAA ACTCTACTAT CCAATATGG
 1441 CCACTTACC AATGCTCTA GAATTTGTT AACGCACTG GAGTAATTT TATGAATAC
 1501 TCGTGTGAT AAGCAAGCG GAGAAATTA TATCAGATC TTGCTCAT AATTATAGA
 1561 TTGTGATTA AGGCTCTTT TAGGCGCAT GCGTGGCTC ATGCTGTAA TCCAGCACT
 1621 TTGATAGCT GAGGCAAGT GATGCTTGA GCTCGGAGT TTGAGAGCAG CTTATCAAC
 1681 AAGTGAAGC TCACTCTCA TTTAAAAA AAAAAGTGG TTTAGGATG TCATCTCTT
 1741 CAGTCTTCA TCATGAGCA AGTCTTTTT TCTCTCTT ATATTGAGC CTCATCTCT
 1801 ACTGCTGTG CATTTAATG ACATCTAAT ACAGATGCG CACAGCCACA ATGCTTTGG
 1861 TTATGTTTT TTAATTTAG AACGGATTA TCTGTTAT ACCTGATTT TCACTTTGG
 1921 ATATTTTTGA CTTAATGAT AGATTATCA GACGTACCG TATGTAAGT CATGAGATA
 1981 TGACTTACG AGGCTTCAG TTAGATTTT GAGCTTAAG ATAGGATTA TGGGGCTTA
 2041 CCGCCACCTT AATTAGAGA AACATTTAT ATTGCTTAC TA

Fig. 1A

RTD 1 --MGLWGQSVPTASSARA--GRYPGARTASGTRPWLLDPKILKFVVFIVA
 DR4 51 GRGALPTSMGQHGPSARARAGRAPGPRPAREASPRLRVHKTFKFV--VVG
 DR5 1 --MEQRGQNAPAASGARKRHG--PGPREARGARPGLRVPKTLVLV--VVA
 DcR1 1 -----MARIPKTLKFVVVIVA

RTD 47 VLLPVRVDSATIPRQDEVPOQTVAPQQQRRSLKEEECPAGSHRSEYTGAC
 DR4 99 VLLQVVPSSAATIKLH---DQSIGTQQWEHSPLGELCPPGSHRSEYTGAC
 DR5 45 VLLLVSASALITQQDLAPQQRAAPQQKRSSPSEGLCPPGHHISEDGRDC
 DcR1 17 VLLPVLAYSATTARQEEVPOQTVAPQQQRHSFKGEECPAGSHRSEHTGAC

CRD1

RTD 97 NPCTEGVDYTIASNNLPSCLLCTVCKSGQTNKSSCTTTRDTCQCEKGSF
 DR4 146 NRCTEGVGYTNASNNLFACLPCTACKSDEEERSPCTTTRNTACQCKPGTF
 DR5 95 ISCKYQDYSTHWNLLFCLRCTRCDSGEVELSPCTTTRNTVCQCEEGTF
 DcR1 67 NPCTEGVDYTNASNNPSCFPCTVCKSDQKHKSSCTMTRDTCQCKEG

CRD2

RTD 147 QDKNSPEHCRTTCRTGCPRGHVKVSNCPTPRSDIKCKNESAAASSTGKTPAAE
 DR4 196 RNDNSAEHCRKCSTGCPRGHVKVKDCTPWSDIECVHKESGNHNIW----
 DR5 145 REEDSPEHCRKCRTGCPRGHVKVGDCPTPWSDIECVHKESGIIIGVTVA--
 DcR1 117 RNENSPEHCRKCSR-CPSGEVQVSNCTSWDDIQCVEEFGANAT-----

Fig. 1B

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RTD      233 RKKFISYLKGICSGGGGGPERVHRVLFRRRSCPSRVPGAEDNARNETLSN
DR4      269 -GGDPKCMDRVCFWRLG-----LLRGPAGAEDNAHNEILSN
DR5      209 --KVLPLYLKGICSGGGGDPERVDR-----SSQRPAGAEDNVLNEIVSI

RTD      283 RYLQPTQVSEQEIQGQELAELTGVTVESPEEPQRLLEQAEAEQCRRRRL
DR4      303 ADSLSTFVSEQQMESQEPADLTGVTQSPGEAQCLLGPAEAEQSRRRRL
DR5      250 --LQPTQVPEQEMEVEQEPAEPTGVNMLSPGESEHLLPEAEAEQSRRRRL

RTD      333 VPVNDAD-----DD-----
DR4      353 VPANGADPTETLMLFFDKFANIVPFDSWDQLMRQLDLTKNEIDVVragta
DR5      298 VPANEGDPTETLRQCFDDFADLVPFDSWEPLMRKLGLMDNEIKVAKAEAA

RTD      340 -----SADISTLLDASATLEEGMAKETIQDQLVGSE
DR4      403 GPGDALYAMLMKWVNKTGRNASIMTLLDALERMEERMAKEKIQDLLVDsg
DR5      348 GHRDTLYTMLIKWVNKTGRDASVMTLLDALETlGERLAKQKIEDHLLSSG

RTD      371 KLFYEEDeAGSATSCL
DR4      453 KFIYLEDGTGSaVSLE
DR5      398 KFMYLEGNADsALS

```

Fig. 1C

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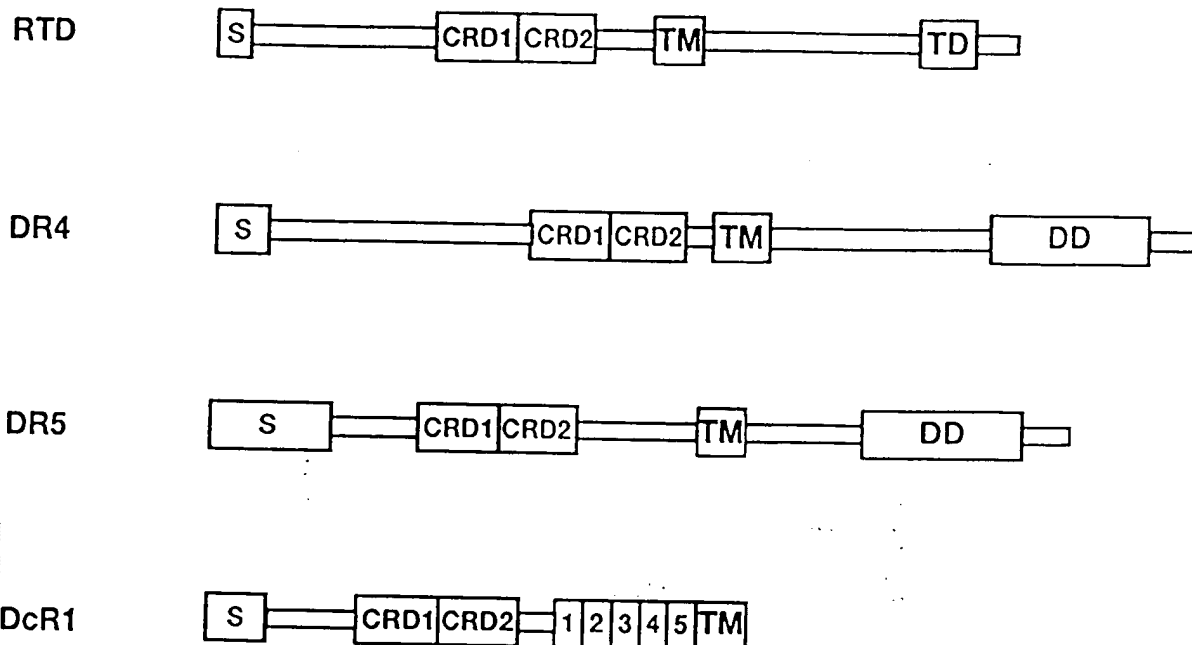
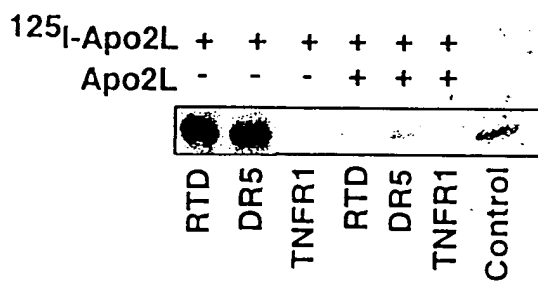


Fig. 1D

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(a)



(b)

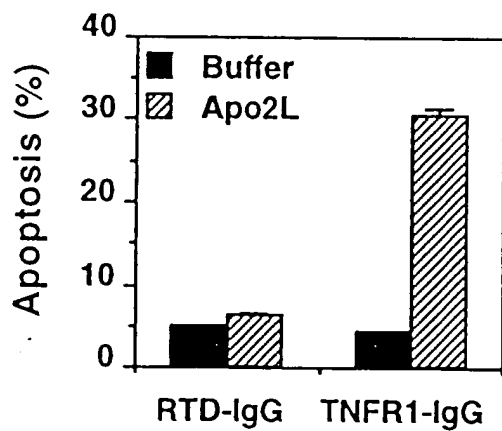


Fig. 2

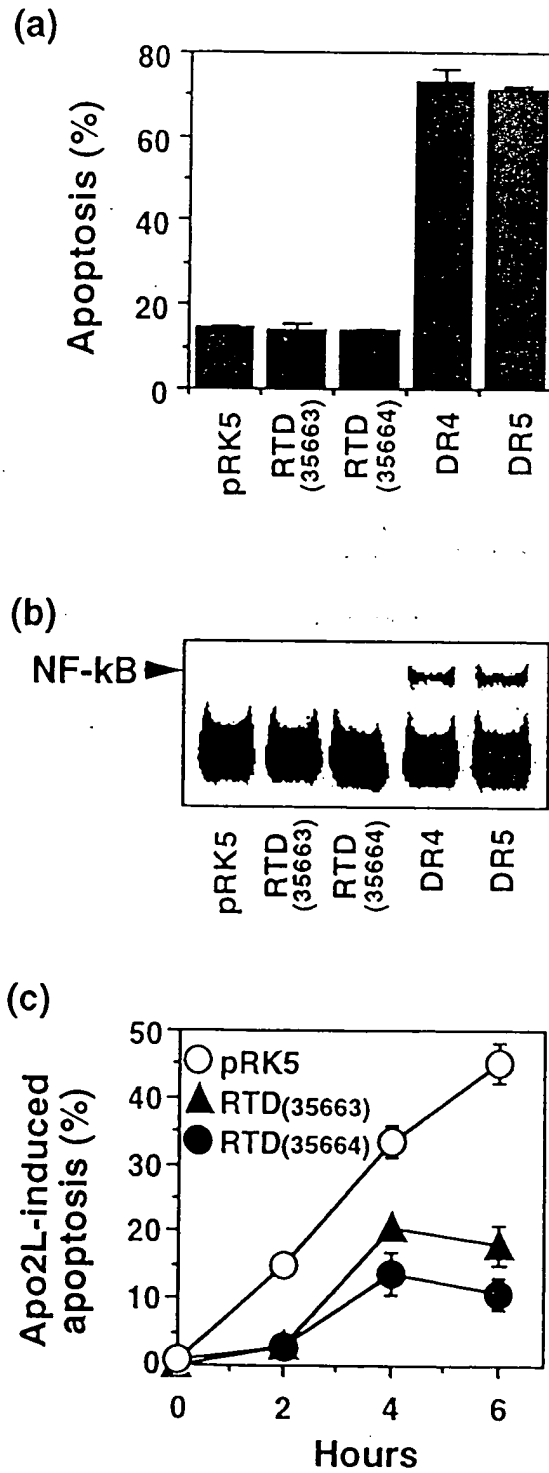


Fig. 3

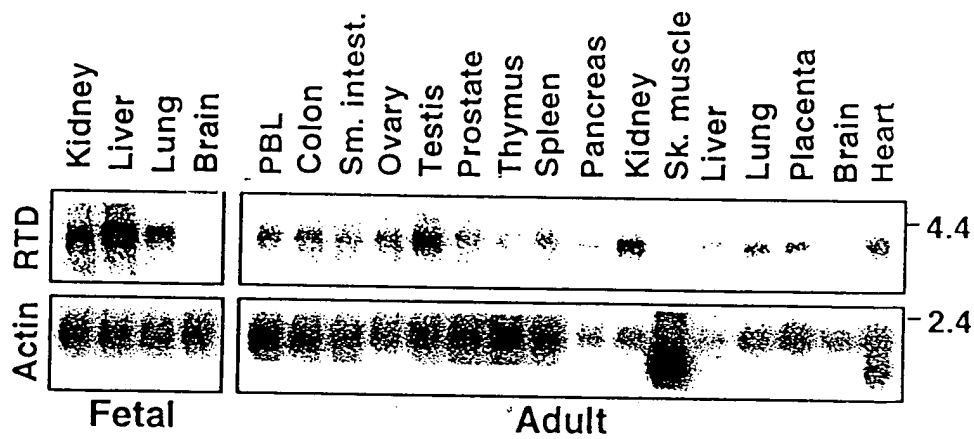


Fig. 4